

EXHIBIT 3

CLUSTAL W (1.83) multiple sequence alignment

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: G_kaustophilus 164 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 75

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05213563.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2667

Alignment Score 773

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05213563.aln]

```

SEQ176      MINRVILVGRLTRDPFELRYTPSGVAVATFTLAVNRPFNTQSYENQEGRRVYVTEVVADSV 60
G_kaustophilus MINRVILVGRLTRDPFELRYTPSGVAVATFTLAVNRPFNTQ----- 40
*****

SEQ176      QFLEPKGTSEQRGATAGGYQGGERETDFIQCVVWRRQAENVANFLKKGSLAGVDGRLQTR 120
G_kaustophilus -----QGERETDFIQCVVWRRQAENVANFLKKGSLAGVDGRLQTR 80
*****

SEQ176      -----GDPFFPGQDQNHQYNEKGF 140
G_kaustophilus SYENQEGRRVYVTEVVADSVQFLEPKGTSEQRGATAGGYGDPFFPGQDQNHQYNEKGF 140
*****

SEQ176      GRIDDDPFANDGQPIDISDDDLPF 164
G_kaustophilus GRIDDDPFANDGQPIDISDDDLPF 164
*****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_cereus 170 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 57

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05263720.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2366

Alignment Score 364

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05263720.aln]

```

SEQ176      MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRR--VYVTEVVAD 58
B_cereus    MMNRVILVGRLT KDPLRYTPNGVAVATFTLAVNRAFANQQGEREADFINCVIWRKQAE 60
             *:*****:****:*****:*****:*****:*****:*****:*****:*****:

```

```

SEQ176      SVQFLEPKGTSEQRGATAGGYQQGERETDFIQCVVWRRQAENVANFLKKGSLAGVDG--- 115
B_cereus    VANYLKKGSLAGVDGRLQTRNYEQ---DGKRVYVTEVLAESVQ-FLEPRNGGGGEQRGSF 116
             .::*: . : * *: * : * . **,* **: . .* :

```

```

SEQ176      RLQTRGDPF-----PFGQDQNHQYPNEKGFGRIDDDFFANDGQFIDISDDDLPF 164
B_cereus    NQQPSGAGFGNQGSNPFQSSNSGNQNSGFTK-NDDPFNSVVGQPIDISDDDLPF 170
             . *. * * ***** .:.* : :*****:*****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_anthraxis 176 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 56

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05321442.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2356

Alignment Score 337

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05321442.aln]

```

SEQ176      ---MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRR--VYVTEV 55
B_anthraxis MVRMLNVRVILVGRLTKDPLRYTPNGVAVATFTLAVNRAFANQQGEREADFNCVIWRKQ 60
              :*****:***:*****.*****.***. **.: . * :

SEQ176      VADSVQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRRQAENVANFLKKGSLAGVDG 115
B_anthraxis AENVANYLKKGSLAGVDGRLQTRNYEGQ---DGKRVYVTEVLAEVSVQ-FLEPRNGGGEQR 116
              . : .:***: . : * *:*: * : * . **.* **: . .* :

SEQ176      ---RLQTRGDPF-----PFGQDQNHQYPNEKGFG--RIDDDPFANDGQPIDISDDDLPF 164
B_anthraxis GSFNQQPSGAGFGNQSSNPFGQSSNSGNGQNSGFTKNDDPFPSNVGQPIDISDDDLPF 176
              . *. * * *****. .:***. :****:* *****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_thuringiensis 173 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 56

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05344058.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2365

Alignment Score 351

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05344058.aln]

```
SEQ176          MINRVILVGRLTRDPFELRYTPSGVAVATFTLAVNREFTNQSVENQEGRR--VYVTEVVAD 58
B_thuringiensis MMNRVILVGRLTKDPLRYTPNGVAVATFTLAVNRAFANQQGEREADFINCVIWRKQAE 60
                  *:*****:***:*****.*****.***. *.: . * : . :

SEQ176          SVQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAENVANFLKKGSLAGVDG--- 115
B_thuringiensis VANYLKKGSLAGVDGRLQTRNYEGQ---DGKRVYVTEVLAESVQ-FLEPRNGGGEQGRGSF 116
                  .::*: . : * *:*: * : * . **.* **: . . * :

SEQ176          RLQTRGDFF-----PFGQDQNHQYPNEKGFG--RIDDDPFANDGQPIDISDDDLFF 164
B_thuringiensis NQOPSGAGFGNQSSNPFQSSNSGNGQGNQNSGFTKNDDPFSSNVGQPIDISDDDLFF 173
                  . * . * * *****. * .::* . :*****: *****
```

```

SEQ176
B_weihenstephanensis
MINRVILVGRRLTRDPRLRYTPSGVAVATFTLAVNRPFTNQSYENQEGRR--VYVTEVVAD 58
MMNRVILVGRRLTKDPLRYTPNGVAVATFTLAVNPAFANQQGGERADDFINCVIWRKQAE 60
*:*****:*:*****.*****.***. *.: . * : . :

SEQ176
B_weihenstephanensis
SVQFLEPKGTSEQRGATAGGYYQGERETDFIQCVVWRRQAEENVANFLKKGSLAGVDG--- 115
VANYLKKGSLAGVDGRLQTRNYDQG---DGKRVYVTEVLAESVQ-FLEPRNGGGEQRGSF 116
.:*: . : * **: * : * . **.* **: . .* :

SEQ176
B_weihenstephanensis
RLQTRGDPF-----PFGQDQNHQYPNEKGFG--RIDDDPFANDGQPIDISDDDLPF 164
NQQPSGAGFGNQSSNPFQGSNSGNQGNQGSQFTKNDPFSNVGQPIDISDDDLPF 173
. *. * * ****.* .:*. :****.* *****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_subtilis 172 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 59

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05422505.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2402

Alignment Score 388

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05422505.aln]

```

SEQ176      MINRVILVGRLTRDPRLRYTPSGVAVATFTLAVNRPFNTQSYENQEGRRVYVT--EVVAD 58
B_subtilis  MLNRVVLVGRLLTKDPELRYTPNGAAVATFTLAVNRFTFTNQSGEREADFINCVTWRRQAEN 60
             *:***:*****:*****:*,*****:*****:***** *: .  ** . . :

SEQ176      SVQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRRQAENVANFLKK-----GSL 110
B_subtilis  VANFLKKGSLAGVDGRLQTRNYENQQGQ---RVFVTEVQAESVQFLEPKNGGGSGSGGYN 117
             ..** :  :  *      *:::  : .* . ***.* :  *      *

SEQ176      AGVDGRLQTRG---DPFPFGQDQNHQYPNEKGFGRIDDDPFANDGQPIDISDDDLPF 164
B_subtilis  EGNSGGGQYFGGGQNDNPFGGNQNRRNQG--NSFNDDPFANDGKPIDISDDDLPF 172
             * . * * * : *** :**:* *: . :*****:*****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_licheniformis 170 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 60

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05435846.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2430

Alignment Score 399

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05435846.aln]

```

SEQ176      MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRR--VYVTEVVAD 58
B_licheniformis MLNRVVLVGRLT KDPELRYTPSGAAVATFTLAVNRTFTNQGGEREADFINCVVWRRQAEN 60
*:***:*****:*****:*****:*****:*****:*****:*****:*****:*****:

SEQ176      SVQFLEPKGTSEQRGATAGGYQQGERETDFIQCVVWRRQAENVANFLKKGSLAGVDGRLQ 118
B_licheniformis VANFLKKGSLAGVDGRLQTRSYENQQGQ--RVYVTEVQAESVQFLEPKGGSGSGGYSG 117
.:**:. : * :*:: : * . **.* : **.* :* .*

SEQ176      TRG-----DFFPFGQDQNHQYFNEKGFGRIDDDPFANDGQPIDISDDDLPF 164
B_licheniformis GQGGQHFGGGQNEPAPFGGSQNNQNRNQ--NSFNDDPFANDGKPIDISDDDLPF 170
:* :* *** .**:* *: . :*****:*****

```


CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_halodurans 168 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 54

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05480066.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2356

Alignment Score 350

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05480066.aln]

```

SEQ176      MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRR-VYVTEVVADS 59
B_halodurans MLNRVVLVGRLTRDPELRYTPNGVAVANFTLAVNRPFSNQGGEREADFINCVWRKQAE 60
              *:***:*****:*****:*****:*****:***. *.: .      * .  *:..

SEQ176      VQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAENVANFLKKGSLAGVDGRLQT 119
B_halodurans VANYLKKGSG--LAGVDGRIQTRSYDNNEGRRVFVTEVMAESVQFLEPRGSQSQGGSNVDN 118
              *      **:      *. .      :.  :.: :.* .  **.* :  :** :  ....:..

SEQ176      RG--DF-FPFGQDQNHQYPNEKG--FGRIDDDPFANDGQPIDISDDDLPF 164
B_halodurans FGGGSPNNPMGGNDFGQQSGGSGRQSGGFSEDPFANDGKPIDISDDDLPF 168
              * . *  *: * : :  * . . *  * :.:*****:*****:*****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ176 164 aa

Sequence 2: B_clausii 161 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 54

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05513189.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:2277

Alignment Score 542

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05513189.aln]

```

SEQ176      MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRRVYVTEVVADSV 60
B_clausii   MLNRVVLVGRLTRDPELRETPNGVAVANFTLAVNRPFSNQ----- 40
*:***:*****:*.*****.*****:*
```

```

SEQ176      QFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAENVANFLKKGSLAGVDGRLQTR 120
B_clausii   -----QGEREADFINCVVWRKPAENVANFLKKGSLAGVDGRVQTR 80
          *****:***:*****: *****:***
```

```

SEQ176      -----GDPFPFGQDQNHQYP---NEKGFGR----- 142
B_clausii   SYDNNEGRRVFVTEIVAESVQFLEPRNSQSSGNNPGFDQYGAGNQSGNQQTGGSRSNG 140
          .... * : : * *      *: **:
```

```

SEQ176      IDDDPFANDGQPIDISDDDLPF 164
B_clausii   YDNDPFNSNDG-SIDISDDDLPF 161
*:***:*** .*****
```